

Table 1S. Scored peptides used to identify proteins by MS using MASCOT. Bold peptides = expectation values (Expect) < 0.05.

Protein <sup>a</sup>	Accession #	Charge	Ion Score	Expect	Peptide Sequence
Hsc70	gi 309319	2	<b>34</b>	<b>0.0086</b>	<b>K.LLQDFFNKG.E</b>
		2	<b>50</b>	<b>0.0051</b>	<b>K.DAGTIAGLNVLRI</b>
		2	<b>53</b>	<b>0.0031</b>	<b>K.VEIIANDQGNR.T</b>
		2	<b>40</b>	<b>0.003</b>	<b>K.MKEIAEAYLGK.T (M oxidation)</b>
		2	22	0.056	R.ARFEELNADLFR.G
		2	<b>85</b>	<b>4.9e-08</b>	<b>R.TTPSYVAFTDTER.L</b>
		3	4	0.98	K.LLQDFFNKELNK.S
		2	16	1.3	K.SFYPEEVSSMVLTK.M (M oxidation)
		2	<b>27</b>	<b>0.038</b>	<b>K.NQVAMNPTNTVFDKR.R (M oxidation)</b>
		3	<b>70</b>	<b>2.8e-06</b>	<b>R.IINEPTAAAIAYGLDKK.V</b>
		3	<b>63</b>	<b>1.4e-05</b>	<b>K.NQVAMNPTNTVFDKR.L (M oxidation)</b>
		3	<b>66</b>	<b>4.7e-06</b>	<b>K.LDKSQIHDIVLVGGSTR.I</b>
ACSL1	gi 729927	2	12	0.68	K.AILDDLLK.L
		2	16	0.43	R.MPELIDIR.Q
		2	<b>68</b>	<b>7.2e-05</b>	<b>K.IGFFQGDRI.L</b>
		2	<b>45</b>	<b>0.0011</b>	<b>K.LAQGEYIAPEK.I</b>
		3	11	1.2	R.IFGQANTSLKR.W
		2	<b>48</b>	<b>0.00017</b>	<b>K.VLQPTIFPVVPR.L</b>
		2	<b>24</b>	<b>0.014</b>	<b>R.LMITGAAPVSATVLTFLR.T (M oxidation)</b>
		3	<b>31</b>	<b>0.0037</b>	<b>R.TAEALDKDGWLHTGDIGK.W</b>
GP78	gi 1304157	2	<b>30</b>	<b>0.029</b>	<b>R.LTPEEIER.M</b>
		2	<b>53</b>	<b>0.0031</b>	<b>R.VEIIANDQGNR.I</b>
		2	18	0.13	K.DAGTIAGLNVMRI (M oxidation)
		3	<b>44</b>	<b>0.00052</b>	<b>R.IINEPTAAAIAYGLDKR.E</b>
FMO5	gi 3334185	2	17	0.08	R.WATQVFK.G
		2	<b>46</b>	<b>0.016</b>	<b>R.SGDIGGLWR.F</b>
		2	<b>43</b>	<b>0.0038</b>	<b>R.IMYYLSR.I (M oxidation)</b>
		3	23	0.27	R.FDHEMFGLKPK.H (M oxidation)
		2	<b>60</b>	<b>1.1e-05</b>	<b>R.ASIYQSVVINTSK.E</b>
		3	<b>40</b>	<b>0.0056</b>	<b>R.DYKNPVEFTGKR.V</b>
		3	<b>46</b>	<b>0.00068</b>	<b>R.ALSQHPTVNDLPLNR.I</b>
Cyp3a11	gi 6681113	2	<b>37</b>	<b>0.018</b>	<b>K.DSIEFFKK.F</b>
		2	<b>70</b>	<b>1.9e-06</b>	<b>R.ALLSPTFTSGK.L</b>
		2	<b>46</b>	<b>0.00082</b>	<b>K.DVELNGVYIPK.G</b>
		3	<b>32</b>	<b>0.0066</b>	<b>K.AISISKDDEWKR.Y</b>
		3	20	1.4	R.QGLLQPEKPIVLK.V
		2	<b>36</b>	<b>0.0027</b>	<b>K.GSIDPYVYLPFGNGPR.N</b>
		3	17	0.38	K.LKEMFPVIEQYGDILVK.Y (M oxidation)
Cyp2d26	gi 13386414	2	<b>53</b>	<b>0.0022</b>	<b>R.FSVSTLR.D</b>
		2	18	0.85	R.RFSVSTLR.D
		2	<b>66</b>	<b>9.5e-05</b>	<b>K.LNSFIALVVK.M</b>
		2	<b>54</b>	<b>0.00014</b>	<b>K.GVILAPYGPEWR.E</b>
		2	11	0.32	R.RFEYEDPFFNR.M
		3	<b>24</b>	<b>0.019</b>	<b>R.VHQEIDEVIGHVR.H</b>

		3	50	0.00025	R.MPYTNAVIHEVQR.F (M oxidation)
UGT1	gi 436187	2	64	0.0002	R.IPQTVLWR.Y
Cyp2d10	gi 387141	2	53	0.0022	R.FSVSTLR.N
		2	24	0.85	R.RFSVSTLR.N
		2	13	0.94	K.KSLEDWVTK.E
		2	70	1.9e-05	R.FGDIAPLNLPR.I
		2	18	0.85	R.DIEVQDFLIPK.G
		2	72	3.4e-06	R.NLTDAFLAEIEK.V
		2	86	1.4e-06	R.VQQEIDAVIGQVR.H
		3	50	0.00025	R.MPYTNAVIHEVQR.F (M oxidation)
Cyp2d9	gi 74180862	2	53	0.0022	R.FSVSTLR.N
		2	24	0.85	R.RFSVSTLR.N
		2	13	0.94	K.KSLEDWVTK.E
		2	47	0.0012	R.TTWDPVQAPR.N
		2	55	0.00011	R.FGDIVPVNLPR.I
		2	72	3.4e-06	R.NLTDAFLAEIEK.A
		2	73	1.4e-05	R.VQQEIDEVIGQVR.H
		3	21	0.26	R.ITSHDIEVQDFLIPK.G
mEH	gi 6753762	2	29	0.17	K.LLAQDIR.K
		2	5	0.097	K.GLNSVATAR.I
		2	50	0.00039	R.ASPPLEGSR.F
		2	23	1.5	K.LLAQDIRK.F
		2	19	0.11	K.IIPLLTDPK.T
		2	41	0.033	K.KGLNSVATAR.I
		2	36	0.0038	K.LISYSYMER.G (M oxidation)
		2	65	6.7e-06	R.NIYSLTPLLQQR.F
		3	21	0.063	K.VFVPTGYSAFPSEILHAPEK.W
IFN	gi 28261389	2	13	1.4	R.ALQFQDLIK.M
GTPase		2	55	0.0018	R.ENLQQAQVR.D
		2	42	0.0012	K.VIGIVKDEIQSK.S
		2	83	1.5e-07	K.VFGVDDGSLQQVAR.S
		3	23	0.12	R.FIGHEEEDSAPTGVVR.T
17β-HSD13	gi 148688291	2	46	0.0032	R.ALTAELDTLKG.T
		2	33	0.012	R.SLINGILTNNK.M
		3	14	0.23	R.IQNIQFEAIVGHK.T
17β-HSD1	gi 633242	2	51	0.0052	R.KIMEFFSLR.Y (M oxidation)
		2	39	0.0013	K.MTQPMIAPYSASK.F (M oxidation)
RDH7	gi 8567342	2	50	0.00098	R.YSAGWDAK.L
		2	57	0.00067	R.TNVSNYER.L
		2	35	0.0034	R.VVNISSSMGR.V
		2	63	0.00032	K.VAIIEPGGFR.T
		2	11	0.72	R.TRYAGWDAK.L
		2	49	0.00053	K.LWDQTSSEVK.E
		2	20	0.23	R.GRVVNISSSMGR.V
		2	36	0.0077	K.TESIVAATQWVK.E

		3	4	6.8	K.YGVEAFSDSLRR.E
		3	12	0.42	K.EVYDKNFLDSYIK.A
Bdh1	gij 20071598	2	38	0.0024	R.VVNISMLGR.M (M oxidation)
		2	67	2.6e-06	K.VSVVEPGNFIAATSLYSER.I
ApoE	gij 192005	2	57	0.00021	R.LGPLVEQGR.Q
		2	36	0.047	R.LQAEIFQAR.L
		2	6	4.3	R.GRLEEVDGNQAR.D
PGRMC1	gij 2801793	2	2	1.6	K.VFDVTK.G
		2	57	8.5e-05	R.ILMAINGK.V (M oxidation)
		2	11	1.9	R.RDFTPAELR.R
		3	37	0.052	K.RRDFTPAELR.R
		2	78	1.7e-07	K.FYGPEGPYGVFAGR.D
		3	26	0.017	R.ILMAINGKVFDVTK.G(M oxidation)
		3	41	0.00038	K.IVRGDQPGASGDNDDEPPPLPR.L
Rtn3-4	gij 16716353	2	8	0.86	K.LPGIAK.K
		2	27	0.093	K.SVIQAVQK.S
		3	56	0.0017	K.TQIDHYVGIAR.D
		3	57	0.00019	K.YKTQIDHYVGIAR.D
		3	33	0.025	K.SIVEKIQAKLPGIAK.K
Gst Pi	gij 1576133	2	49	0.00042	K.FEDGDLTYQSNAIR.H
		3	17	0.26	K.ALPGHLKPFETLLSQNQGGK.A
Mett17b	gij 19354269	2	18	3.1	R.AFLWQR.V
		2	16	0.53	R.VLEPTWK.H
		2	31	0.46	R.ETWKDIER.A
		2	38	0.092	R.ELFSQIKDLK.G
		3	7	2.3	R.WLPVGP HIMGK.A (M oxidation)

<sup>a</sup>Hsc70, Heat Shock Protein 70 cognate; ACSL5, Long-chain fatty acid-CoA ligase 1; GP78, 78 kDa glucose-regulated protein; FMO5, Dimethylaniline monooxygenase 5; Cyp, cytochrome P450; UGT1, UDP-glucuronosyltransferase, family 1; mEH, Epoxide hydrolase 1, microsomal; IFN GTPase, Interferon- $\gamma$ -induced GTPase; 17 $\beta$ -HSD1, 17 $\beta$ -hydroxysteroid dehydrogenase 13; 11 $\beta$ -HSD, 11 $\beta$ -hydroxysteroid dehydrogenase;..RDH7, Retinol Dehydrogenase 7; bdh1, 3-hydroxybutyrate dehydrogenase, type 1; ApoE, Apolipoprotein E; PGRMC1, Progesterone Receptor Membrane Component; RTN3-4; reticulon-3 isoform 4; GST Pi, Glutathione S-transferase, Class Pi; Mettl7b, methyltransferase-like 7b.